# SEQUENCE LISTING

GENERAL INFORMATION: (1)

(i) APPLICANT:

Lebrun, Michel Sailland, Alain Freyssinct, Georges DeGryse, Eric

(ii) TITLE OF INVENTION: Mutated 5-enolpyruvylshikimate-3-phosphate synthase, gene coding for this protein and transformed plants containing this gene

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Connolly, Bove, Lodge and Hutz

(B) STREET: 1220 Market Street

(C) CITY: Wilmington

(D) STATE: Delaware

(E) COUNTRY: U.S.A.

(F) ZIP: 19899

#12

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:

(B) COMPUTER:

(C) OPERATING SYSTEM:

(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/FR96/0112/

(B) FILING DATE: 18-JUL-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Robert G. McMorrow, Jr.

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (302) 658-9141

(B) TELEFAX: (302) 658-5614

### (2) INFORMATION FOR SEQ ID NO:3/2

### (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1713 Sees pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: /inear

(11) HOLECULE TYPE: CONA

(vi) ORIGINAL BOURCE:
(A) ORGANISM: See mays
(B) STRAIN: Black Mexican Sweet

(7) TIBSUE TYPE: Callus

(V11) DAGBIATE BOUNCE:

(A) LIBRARY: lambda gt10

(B) CLOME: pRPA-HL-711

### (xx) SEQUENCE DESCRIPTION: AEQ ID MO:1:

,						
MTCMTTTC	<b>ACACAGONA</b>	CAGCTATGAC	CATGATTACS	AATTOGGGCC	COGOCOCOTO	60
ATOCOGOGO	GCAGCEGCS	G00000079C	A0000007100	COMOGRAÇATO	GTGCTGCAGC	120
CATCAAGGA	CATCTCCGGC	ACCORTONAC	T0000000TC	CAMPTOGETT	TOCALCOSSA	180
TOCTOCTACT	00000000000000000000000000000000000000	TOOSAGGGGA	CALCUSTOST	TGATAACCTG	CTGAACAGTG	240
ASCATOTOCA	CTACATGCTC	GGGGCCTTGA	GGACTCTTGG	TCTCTCTOTC	GAAGCOGACA	300
AUGCTGCCAA	AAGAGCTGTA	оттоттоост	GTGGTGGAAA	<b>ellocorti</b>	GAGGATOCTA	360
NENGGANGT	OCADCTCTTC	TTGGGGAATG	СТОВЛАСТОС	AATOCOGCCA	TTGACAGCAG	420
COCOO ACOUNT	2002002004		A	**********	AGA MCAGG	480

MININCECAT TERMINACTER CENTERGAT TRANSPORT TERMINACTE CONTRACTORT	540
TODITIVICAC TRACTICIDAS CONTROLOS TONATIGIANT COGASSACTA CONGOLOGIA	400
AUSTONAGGE GEGEFFESTON AFGARCANTO AGEACTICAG TOCCTTOCHG ATGGCTCCTC	640
CITTIVECTOR TEXESPANTED GASATITGAAA TOATTGATAA ATTAATOTOO ATTOCGTACG	720
TOGANATGAC ATTGAGATTG ATGGAGOTTT TTGGTGTGAA AGCAGAGGAT TCTGATAGCT	780
COGACAGATT CTACATTAAG GGAGGTCAAA AATACAAGTC CCCTAAAAAT GCCTATGTTG	840
AAGGTGATGC CTCAAGCGCA AGCTATTICT TGGCTGGTGC TGCAATTACT GGAGGGACTG	900
TEAUTETEEA AUGTTUTEGC ACCACCAST? TECASOSTEA TETEGAAGTT? GCTGAGGTAC	960
TGGAGATGAT GOGAGCGAAG GTTACATGGA CCGAGACTAG CGTAACTGTT ACTGGCCCAC	1020
COCEGGRAGOC ATTTGGGRAGG AMACACCTCA AGGCGATTGA TGTCAACATG AACAAGATGC	1020
CTGATGTOSC CATGACTCTT OCTGTGGTTG COCTCTTTGC CGATGGCCCG ACAGCCATCA	1140
GAGACITIOSC TICCIGGAGA GIAAAGGAGA COGAGAGGAT GGTTGCGATC COGACGGAGC	1200
TANCENAGET GGGAGCATET GTTGAGGAAG GGGCGGAGTA CTGCATCATC ACGCCGGCGG	1260
AGAAGGTGAA COTGACHGCS ATCGACHGCT AGGACGAGCA CAGGATGGCC ATGGGCTTCT	1320
CONTIGORIC CTGTGCCCAG GTCCCCCTCA CCATCCGGGA CCCTGGGTGC ACCCGAAGA	1380
CTTCCCCGA CTACTTCGAT GTGCTGASCA CTTTCGTCAA GAATTAATAA AGGSTGCGA?	1440
CTACCACCC ASCTTGATTG AAGTGATAGG CTTGTGCTGA GGAAATACAT TTCTTTTGTT	
REGITTITICS CTTSCACOGG ATTANGETTS GAGICTGIAA COTTAGETGT TESTAGCAAG	1500
TIGIATTIC GGATCITAAG TITGIGCACT GTAAGCCAAA TTTCATFTCA AGAGTGGTTC	1560
TIGGANTAN TANGAATRAT AAATTAGGT TONGTON AMAAAAAA AAAAAAAA	1620
MANANA AMANANA MCCCCCCAN TTC	1680
21 YHERMANATAN	1713

- (2) INFORMATION FOR SEQ ID NO.2:
  - (1) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1340 base pairs
      (B) TYPE: nucleic scid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (11) MOLECULE TYPE: CONA
  - (V1) ORIGINAL SOURCE:

    - (A) ORGANISM: Zee Says (B) STRAIN: Slack Mexican Sweet
  - (vii) Decolate source: (8) CLOME: prpa-ML-716
  - (ix) FEATURE:

    - (A) NAME/KEY: CDS (B) LOCATION: 6..1337
  - (x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATG GCC GGC GCC GAG GAG ATC GTG CTG CAG CCC ATC AAG GAG ATC Ale Gly Ale Glu Glu Ile Val Leu Gln Pro Ile Lye Glu Ile 1	47
TOO GGC ACC GTC AAG CTG CCG GGG TCC AAG TCG CTT TCC AAC CGG AT Ser Gly Thr Vel Lye Leu Pro Gly Ser Lye Ser Leu Ser Aen Arg II 15 20 25 3	PC 95
CTC CTA CTC GCC GCC CTG TCC GAG GGG AGA ACA GTG GTT GAT AAC CT Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Vel Asp Asn Le 35 40	G 143

191

CTG AAC AGT GAG GAT GTC CAC TAC ATG CTC GGG GCC TTG AGG ACT CTT Lou Aen Ser Glu Aep Val His Tyr Het Leu Gly Ale Leu Arg Thr Leu

50	55	40	
GTT CTC TCT TTC GAA GCT G GLY Law Sar Val GLU ALS A 69	20 LAS VIT VIT	Lys Arg Ala Val Val Val	
	85	Aid Lya Glu Glu Val Gla 90	287
CTC TTC TTG GGG AAT GCT GK Leu Phe Leu Gly Aen Ala GI 95 100	A TUL VIE MEE	Arg Pro Leu Thr Ala Ala 105 110	335
OTT ACT OCT GCT GGT GGA AN Val Thr Ala Ala Gly Gly As 115	120	Val Leu Amp Gly Val Pro 125	383
AGA ATG AGG GAG AGA COC AT Arg Het Arg Glu Arg Pro II 130	135	Val Val Gly Lau Lys Gln 140	431
CTT GGT GCA GAT GTT GAT TG Leu Gly Ale Asp Val Asp Cy 145	150	Thr Asp Cyr Pro Pro Val	479
CGT GTC AAT GGA ATC GGA GGG Arg Vel Asn Gly Ile Gly Gly 160 161	L CAO LEG GIÀ	Gly Lys Val Lys Leu Ser 170	527
GGC TCC ATC AGC AGT CAG TAG Gly Ser Ile Ser Ser Gln 2yr 175 180	Fed Bet VIT	Leu Leu Net Ale Ale Pro 190	575
TTG GCT CTT GGG GAT GTG GAG Lou Ala Lou Gly Asp Val Glu 195 ATT CCG TAC GTC GAA ATG ACA Ile Per Tyr Val Glu Hee Tac	200	le Amp Lyw Leu Ile Ser 205	623
Ile Pro Tyr Val Glu Het Thr 210 AAA GCA GAG CAT TCT GAT AGC	212 212	et Glu Ary Phe Gly Val 220	671
225	230 Asp Arg P.	he Tyr Ile Lys Gly Gly 235	719
CAA AAA TAC AAG TCC CCT AAA Gln Lym Tyr Lym Ser Pro Lym 240  AGC GCA AGC TAT TTC TTG GCT Ser Als Ser Tyr Pho Lou Dlo	Was vie the A	250 250 Asp Ala Ber	167
255 260	OTA VIE VIE II	te Thr Gly Gly Thr Val 270	815
ACT GTG GAA GGT TOT GGC ACC Thr Vel Glu Gly Cye Gly Thr 275	280	in Gly Amp Val Lym Phe 285	863
GCT GAG GTA CTG GAG ATG ATG ATG ATG ATG GTU Vel Leu Glu Net Net 280	295	1 The Trp The Glu The 300	913
	110 VIA CIA by	o Phe Gly Arg Lys His 315	959
CTC AND GCG ATT GAT GTC AND ; Lou Lye Ala Ile Asp Vel Asn ; 320 328	ot Am Lys Me	t Pro Asp Val Ala Met 330	1007
ACT CTT GCT GTG GTT GCC CTC TT THE Leu Ale Vel Vel Ale Leu 6 335 340	341 Ma vrs vsb GT	y Pro Thr Ala Ile Arg 380	1055
GAC GTG GCT TCC TGG AGA GTA A Asp Val Alm Ser Trp Arg Val 1 355	360	Arg Met Vel Ala Ila 365	1103
CGG ACE GAG CTA ACC AAG CTG G Arg Thr Glu Leu thr Lys Lsu G	GA GCA TOT GTT ly Ale Ser Vel	GAS GAA GGG CCO GAC	1151

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### (2) INFORMATION FOR SEQ ID NO:3:

### (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 sains scids
- (B) TYPE: amino sold (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

### (x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ale Gly Ale Glu Glu Ile Vel Leu Gln Pro Ile Lye Glu Ile Ser Gly 1 5 10 15

Thr Val Lys Lau Pro Gly Ser Lys Ser Lau Ser Asn Arg Ile Lau Lau 20 25 30

Leu Als Als Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn 45

Ser Glu Asp Val His Tyr Net Leu Gly Ala Leu Arg Thr Leu Gly Leu 50 55 60

Ser Val Glu Ala Aap Lys Ala Ala Lys Arg Ala Val Val Gly Cys 65 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe 85 90 93

Leu Gly Asn Ala Gly Thr Ala Net Arg Pro Leu Thr Ala Ala Val Thr

Ala Ala Oly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met 115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Vel Gly Leu Lys Gln Leu Gly 130 135 140

Alm Amp Val Amp Cym Phe Lau Gly Thr Amp Cym Pro Pro Val Arg Val 145 150 150 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lye Val Lye Leu Ser Gly Ser 165 170 175

Ile Ser Ser Gln Tyr Lou Ser Ala Lau Leu Met Ala Ala Pro Leu Ala 180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lye Leu Ile Ser Ile Pro 195 205

Tyr Val Glu Het Thr Leu Arg Leu Het Glu Arg Phe Gly Val Lye Ala 210 225 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lye Gly Gly Gln Lys 225 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala 245 250 255

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GD.	GL	γ Cγ:	e 731.y 4	'the	'the	Sec	2330 (A) U	Gin	GLY	/ Asp	Val	Ly:		Ala	Glu	
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1h s 305	Va	1 7h	. uTA	Ptu	Pro 310	Arg	Glu	Pto	Phe	G1y 315	Arg	Lys	Hie	Leu	Lys 320	
Ala	. 11	• Asp	V#1	Asn 325	Het	Asn	Lys	Net	Pro 330	Aup	Va1	Al =	Met	Thr 335	Leu	
Ala	Va	l Val	Ala 340	Leu	Phe	Ala	Asp	G1y 345	Pro	Thr	ALE	Ile	Arg 350	Asp	Val	
Ala	Sei	7.Tp 355	Arg	Val	Lys	Glu	Thr 360	alu	Arg	Met	Val	시1 365	Il•	Arg	The	
Glu	Let 370	The	Lya	Leu	Gly	Ala 375	Ser	Val	<b>G</b> lu	Glu	Gly 380	Pro	Asp	7yr	Cys	
11e 385	Ile	The	\$ to	510	Glu 390	Lys	Lau	Asn	Va1	Thr 395	Ala	Il=	Asp	The	TYF 400	
Asp	Asp	His	Arg	Mat 405	Al.	Met	Ale	Phe	8es 410	Leu	Al <sub>i</sub> a	Ala	Cys	Als 415	Glu	
Val	Pro	Val	7hs 420	Ile	Arg	Asp	Pro	Gly 425	Cys	Thr	ΑſΨ	Lys	2hs 430	Phe	Pro	
Asp	?yr	Pho 435	Asp	Val	Leu	Ser	Thr 440	Phe	Va1	Lyp	Asn					
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CTC ( Leu 1	ATA JOU	cic ( Leu )	BOC G	CC C La L 35	TO T	er d	AG G	GG A	CA A hr 7 40	CA e hr V	7G G al V	TT G	AT A	AC C ISD L 45	77G ÆU	16
CTG A Leu A	UC.	AGT ( Ser (	ias d ilu a 50	at G	TC C	ac t is t	yr H	TG C et L 55	tc a eu a	ac c	∝ t lu L	ou A	GG A Ly 1	er c hr L	TT ØU	19:
ior c	TC 1	ict d Ser v	ric G /el G	AA G lu A	ya Y Ce C	ab r	AA G yo A 70	CT G	OC A	AA A yo A	tà Y	CT G 1. V 75	TA G	TT G	77 al	23

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											ال تاراح تاراح					287
											TOC Sec					135
GTT Val	ACT The	GCT Als	OCT ALB	GIY	GGA Gly	AAT Aan	GCA Ala	ACT Thr	TAC Tyr 120	ord Val	CTT Leu	GA'Ê Asp	OJA OJA	GTA Val 125	CCA Pro-	383
AGA Arg	ATG Het	AGG Arg	GAG Glu	AGA Arg	ccc	ATT Ile	GGC Gly	GAC Asp	TTG	GTT Vel	GTC Val	GGA Gly	TTG Leu	AAG	CAG Gln	431
_	CCT	CCA	130	<b></b>	GAT	TOT	170	135	995	ACT	ø <b>x</b> c	TGC	140 CCA	CCT	GTT.	479
Leu	Gly	Ala 145	Asp	Va 1	Asp	Сув	Phe 150	Leu	Gly	Thr	Asp	Cys 155	Pro	Pro	Va1	
											170					527
											CTG Leu					575
TTG Leu	gct Ale	CTT Leu	GGG Gly	GA7 Asp 195	gig Val	g <b>a</b> g Glu	ATT Ile	Glu	ATC Ile 200	ATT Ile	GAT Asp	AAA Lys	TTA Lou	ATC 110 205	TCC Ser	623
											GAG Glu					671
											tac tyr					719
CAA Gln	AAA Lyb 240	TAC Tyr	AAG Lys	TCC Ser	eci Pro	AAA Lys 245	aat Aan	GCC Ala	TAT Tyr	GTT Val	GAA Glu 250	GGT Gly	gat Asp	AL:	TCA Ser	767
255 8er 255	GCA Ala	AGC Ser	TAT Tyr	TTC Phe	TTG Leu 260	get Als	GOT Gly	GCT Ala	AL a	ATT 110 265	ACT The	GGA Gly	01 y GGG	ACT Thr	G1G Val 270	815
ACT The	GTG Val	GAA Glu	GGT Gly	TGT Cyn 275	GGC Gly	ACC Thr	ACC Th <i>I</i>	<b>?EA</b> 108	TTG Leu 280	CAG Gln	GIY	gat Asp	GTG Val	AAG Lys 283	TTT Pho	863
ALS ALS	G <b>AG</b> Glu	GTA Val	CTG Leu 290	<b>GN</b> 3	ATG Met	ATG Het	GGA Gly	GCG Al = 295	AAG Lys	GTT Val	ACA Thr	TGG Trp	ACC Thr 300	GAG Glu	ACT Thr	911
AGC Ser	OTA Val	ACT Thr 305	GII Val	ACT Thr	gj y GGC	CCA Pro	Pro 310	Arg	GRG Glu	633 019	TTT Phe	GGG Gly 315	AGG AEG	TA2 YYY	CAC His	959
CTC Leu	Lys 320	GCS Als	ATT [16	CAT Amp	OTC Val	AAC Asn 325	ATG Met	AAC Aan	aag Lys	ATG Not	CCT Pro 330	GAT Asp	GTC Vel	GCC Ala	ATG Met	1007
ACT The 335	CTT	A) a	978 Val	GTT Val	000 Ala 340	CTC CTC	TTT Phe	dCC Ala	GA? Asp	GGC Gly 345	500 500	ACA The	A) a	ATC 11s	AGA Arg 350	1055
GAĆ Asp	oro Val	GCT Ala	TCC Ser	760 7rp 355	ADA Arg	OTA Val	AAG Lys	G1u	7hr 360	Glu Glu	yrd Ygg	ATG Het	GTT Vel	906 Ala 365	ATC Ile	1103
Arg	ACG Thr	GAG Glu	CTA Leu 370	ACC Thr	AAG Lys	C7G Leu	gga Gly	60A Ale 375	er 9er	GTT Vel	GAG Glu	GAA Glu	666 617 380	COG Pro	GAC Asp	1151
TAC Tyr	TGC Cys	ATC 110 385	ATC Ile	ACG Thr	Pro	Pro	G)u 310	Lys	ren C10	AAC Ash	GTG Val	ACG Thr 395	YT.	ATC Ile	GAC Amp	1199

ACC TAC CAC GAC CAC ANS ATC GCG ATG GCC TTC TCC CCT GCC CCT TGT
The Tyr Aup Aup Hix Ard Net Ala Net Ala Phe Ser Leu Ala Ala Cys
400

GCC GAC GTC CCC GTC ACC ATC GCG GAC CCT GGG TGC ACC CGG AAG ACC
ALA GIU Val Pro Val The 11e Ard Aup Pro Gly Cys The Arg Lya The 120

TTC CCC GAC TAC TTC GAT GTG CTG AGC ACT TTC GTC AAG AAT Phe Pro Amp Tyr Phe Amp Val Leu Ser The Phe Val Lys Amn

1317

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### (2) INFORMATION FOR SEQ ID NO:5:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 444 emino seide
  - (8) TYPE: smino scid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE MESCRIPTION: SEQ ID NO:5:

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lye Glu Ile Ser Gly
1 5 10 15

Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu 20 25 30

Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn 35 40 45

Ser diu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Lau 50 55 60

Ser Vel Glu Ale Asp Lys Ale Ale Lys Arg Ale Vel Vel Vel Gly Cym 65 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe 85 90 95

Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu 7hr Ala Ala Val Thr 100 105 110

Als Als Gly Gly Asn Als Thr Tyr Val Leu Asp Gly Val Pro Arg Net 115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lym Gln Leu Gly 130 140

Ala Asp Vel Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Vel Arg Vel 145 150 155 160

Agn Gly Ile Gly Gly Lau Pro Gly Gly Lys Val Lys Leu Ser Gly Ser 165 170 175

Ile Ser Ser Gln Tyr Leu Ser Als Leu Leu Net Ala Ala Pro Leu Ala 180 185 190

Lau Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Lau Ile Ser Ile Pro 195 200 205

Tyr Vel Glu Net Thr Lau Arg Lau Net Glu Arg Phe Gly Val Lys Ale 210 225 220

Glu His Ser Asp Ser 7rp Asp Arg Phe Tyr Ile Lye Gly Gly Gln Lye 225 235 240

Tyr Lys Ser Pro Lys Ash Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala 245 250 255

Ser Tyr Phe Leu Ale Gly Ala Ale Ile Thr Gly Gly Thr Vel Thr Vel 265 270

Glu Gly Cys Gly Thr Thr Ser Lau Gln Gly Asp Val Lys Phe Ala Glu 275 280 285

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